

Tnp1 recognized target (TRT)

A TRT' (244bp)

GGTACCGCCAGCATTTTCGGAAAAAAACCACGCTAAGAAAAATCAGAGTTAAAA
 AATCAGAAAAATATATCATTATTCAGACACATACAGTGTCTTTTTTATACAA
 AAAATAATACAACAATATTAATTGTGTTGTATTAGGTGTTATAATA
 AATATAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATAAAT
 ACTTTTAGACGCAACACAATTTATAGACGCGGAGGAAATCAC

B TRT' (116bp)

TAATACAACACAATATTAATTGTGTTGTATTAGGTGTTATAATAAATA
 TAAATCTAGGGGTTTAACGCAACACAATTTATCGATAAATAAATACTTT
 TAGACGCAACACAATTTATAGACGCGGAGGAAATCAC

C TRT (32bp)

TAATACAACACAATATTAATTGTGTTGTATTA

000543.053001

FIG. 1A-C

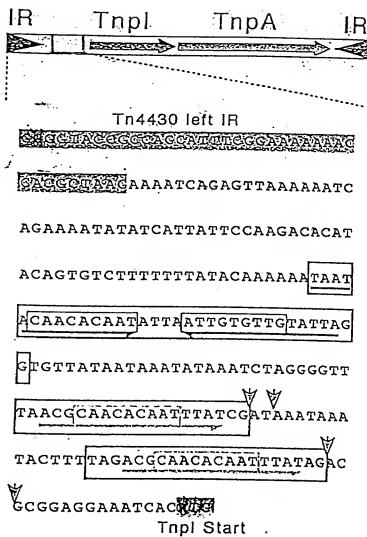
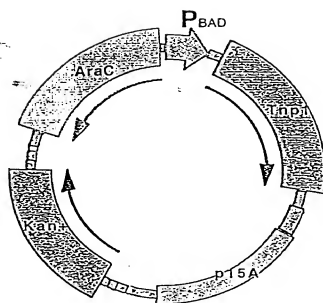


FIG. 2

1 ATG GAT GTT GCA AAA CAG TTE TCT TCT TAT CTT AAA CAA GAG AAT AAA ACC GAG AAC
 19 Met Asp Val Ala Lys Gln Phe Ser Ser Tyr Leu Lys Gln Glu Asn Lys Thr Glu Asn
 58 ACT GTT CAG GGA TAC ACA TCA GGT ATT AGA CAG TAC ATA AAA TGG TTT GAA GGT TCC
 20 Thr Val Gln Gly Tyr Thr Ser Gly Ile Arg Gln Tyr Ile Lys Trp Phe Glu Gly Ser
 115 TAT GAC AGA AAA TTA ACA AAA TTG TAC CGA CAA AAT ATC TTA GAG TAC ATT AGT TAT
 39 Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg Gln Asn Ile Leu Glu Tyr Ile Ser Tyr
 172 TTA AAG AAT GTC AAA ATG TTG AAC GCC AAG TCC ATT AAC CAC AAG ATT AGT AGC CTT
 58 Leu Lys Asn Val Lys Met Leu Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu
 229 GCT AAA TTT AAT GAA TTT CTA ATA CAG AAA GGA AGT CAA CAA GAT CAA GTA ATT TTA
 77 Ala Lys Phe Asn Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu
 286 AAA ACA GAC ATG ATA AAG GTT CAA ACT GTC TAT GCT TCT CCA ACC CAA ATT GTT GAA
 96 Lys Thr Asp Met Ile Lys Val Gln Thr Val Tyr Ala Ser Pro Thr Gln Ile Val Glu
 343 TTA GAT GTA AAA AAG TTT TTA CAA AGT GTG TTA GAG GAT AAT AAC AAA CGT AAT TAT
 115 Leu Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg Asn Tyr
 400 GCA ATT GCC ACT CTC CTA GCA TAT ACA GGA GTA CGT ATT TCA GAG GCA TTA TCT ATC
 134 Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser Glu Ala Leu Ser Ile
 457 AAA ATG AAT GAC TTC AAT TTA CAG ACT GGG GAA TGT ATT ATT CGA AGT GGA AAA GGA
 153 Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu Cys Ile Ile Arg Ser Gly Lys Gly
 514 GGT AAA CAA CGA ATT GTA TTA CTA AAT AGT AAG GTA CTT AGT GCT ATC AAA GAT TAT
 172 Gly Lys Gln Arg Ile Val Leu Leu Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr
 571 CTC ATC GAT CGA AAA ACA TAC AGT ACA GCA CAT GAA TCT CCG TAT CTT TTT ATT AGT
 191 Leu Ile Asp Arg Lys Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser
 628 AAA AAG CGA GAA AAG CTC GAC CGT ACG GTC GTC AAT CGT ATC TTT AAA TCA TAC AGC
 210 Lys Lys Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr Ser
 685 AAT GTT ATT ACT CCA CAC CAA TTA CGA CAC TTC TTC TGT ACG AAT GCA ATT GAA AAA
 229 Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn Ala Ile Glu Lys
 742 GGA TTT ACG ATT CAT GAA GTT GCA AAT CAA GCT GGG CAC TCT AAC ATC CAT ACG ACA
 248 Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly His Ser Asn Ile His Thr Thr
 799 CTT TAC ACA AAT CCA AAC CAA CTG CAG CTA AAA AAT AAA ATG GAG CTC TTA TAA
 267 Leu Leu Tyr Thr Asn Pro Asn Gln Leu Gln Leu Lys Asn Lys Met Glu Leu Leu ...

FIG. 3

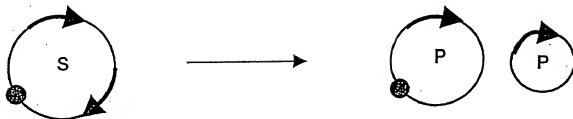


pYZ-BAD-Tnp1
4746bp

FIG. 4

00895435-063001

A



B

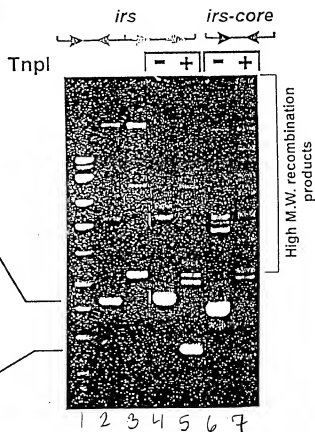


FIG. 5A-B

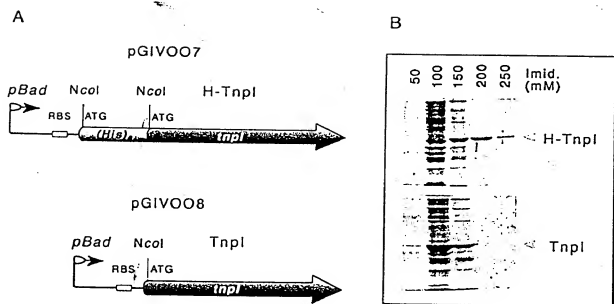


FIG. 6A-B

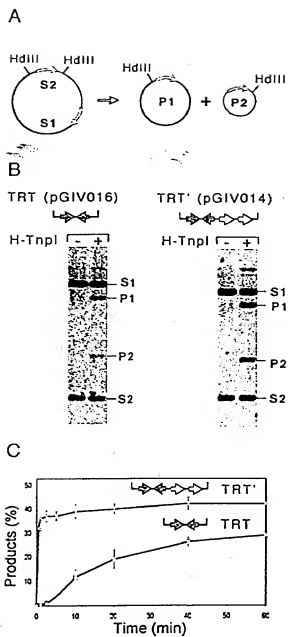


FIG. 7A-C

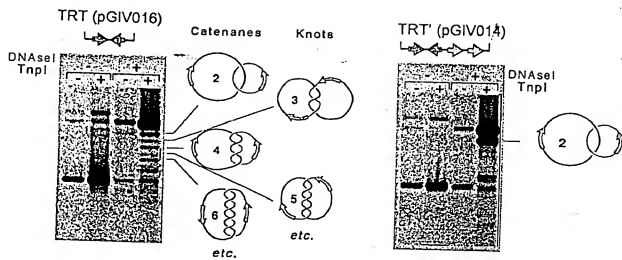


FIG. 8

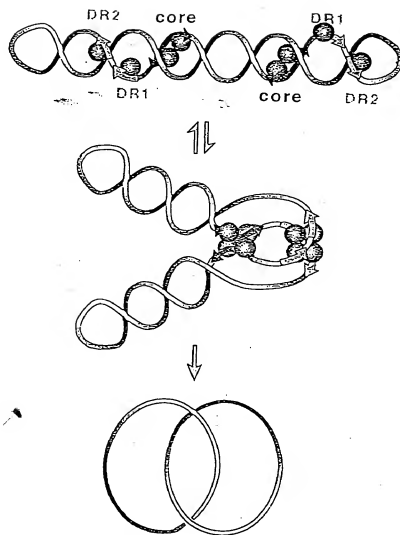


FIG. 9

00895435-062001

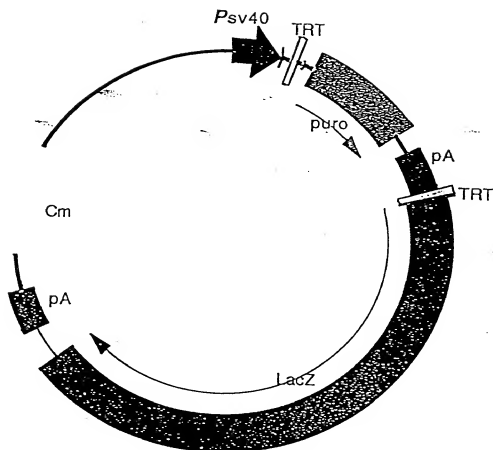


FIG. 10

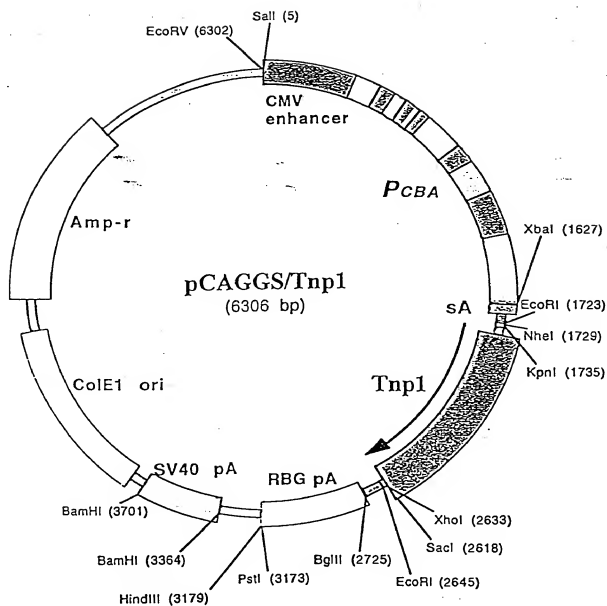


FIG. 11

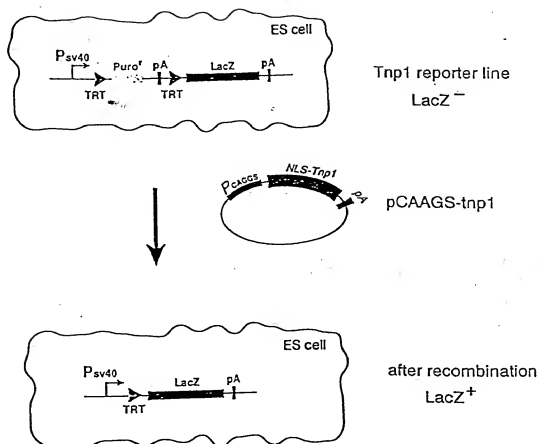


FIG. 12

T00290-55456860

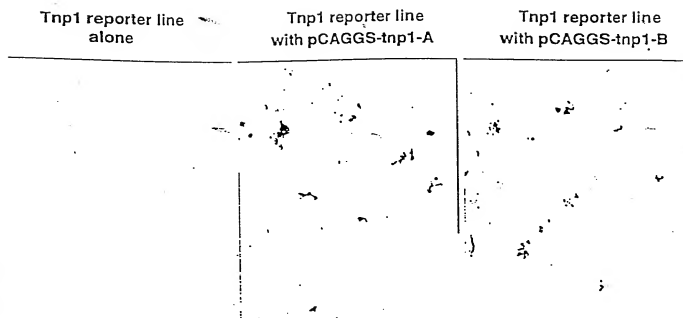


FIG. 13